Application No: 10547206   Version No: 2.0

Input Set:

Output Set:

            Started: 2008-07-31 16:00:40.207
           Finished: 2008-07-31 16:00:42.268
            Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 61 ms
     Total Warnings: 59
       Total Errors: 0
No. of SeqIDs Defined: 62
  Actual SeqID Count: 62

Error code   Error Description

W   213   Artificial or Unknown found in <213> in SEQ ID (3)

W   213   Artificial or Unknown found in <213> in SEQ ID (4)

W   213   Artificial or Unknown found in <213> in SEQ ID (5)

W   213   Artificial or Unknown found in <213> in SEQ ID (6)

W   213   Artificial or Unknown found in <213> in SEQ ID (7)

W   213   Artificial or Unknown found in <213> in SEQ ID (8)

W   213   Artificial or Unknown found in <213> in SEQ ID (9)

W   213   Artificial or Unknown found in <213> in SEQ ID (10)

W   213   Artificial or Unknown found in <213> in SEQ ID (11)

W   213   Artificial or Unknown found in <213> in SEQ ID (12)

W   213   Artificial or Unknown found in <213> in SEQ ID (13)

W   213   Artificial or Unknown found in <213> in SEQ ID (14)

W   213   Artificial or Unknown found in <213> in SEQ ID (15)

W   213   Artificial or Unknown found in <213> in SEQ ID (16)

W   213   Artificial or Unknown found in <213> in SEQ ID (17)

W   213   Artificial or Unknown found in <213> in SEQ ID (18)

W   213   Artificial or Unknown found in <213> in SEQ ID (19)

W   213   Artificial or Unknown found in <213> in SEQ ID (20)

W   213   Artificial or Unknown found in <213> in SEQ ID (21)

W   213   Artificial or Unknown found in <213> in SEQ ID (22)

Input Set:

                    Output Set:

                    Started: 2008-07-31 16:00:40.207
                   Finished: 2008-07-31 16:00:42.268
                    Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 61 ms
           Total Warnings: 59
             Total Errors: 0
    No. of SeqIDs Defined: 62
      Actual SeqID Count: 62

Error code   Error Description

                    This error has occured more than 20 times, will not be displayed

W   402   Undefined organism found in <213> in SEQ ID (59)

W   402   Undefined organism found in <213> in SEQ ID (60)

W   402   Undefined organism found in <213> in SEQ ID (61)

SEQUENCE LISTING

<110> Jacquet, Alain

<120> Hypoallergenic Der p1 and Der p3
    Proteins From Dermatographoides Pteronyssinus

<130> VB60107

<140> 10547206
<141> 2006-05-19

<150> PCT/EP2004/001850
<151> 2004-02-24

<150> 00304424.5
<151> 2003-02-26

<160> 62

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 909
<212> DNA
<213> Dermatophagoides pteronyssinus

<400> 1
cggccgagct ccattaagac cttcgaggaa tacaagaaag ccttcaacaa gagctatgcc 60
accttcgagg acgaggaggc cgcgcgcaag aacttcctgg aaagcgtgaa atacgtgcag 120
agcaacggcg gggctataaa tcacctgtcc gacctgtctt tagacgagtt caagaaccgg 180
ttcctgatga gcgccgaggc tttcgaacac cttaagaccc agtttgatct caacgcggag 240
accaacgcct gcagtatcaa cggcaatgcc cccgctgaga ttgatctgcg ccagatgagg 300
accgtgactc ccatccgcat gcaaggcggc tgcgggtctt gttgggcctt ttcaggcgtg 360
gccgcgacag agtcggcata cctcgcgtat cggaatcaga gcctggacct cgctgagcag 420
gagctcgttg actgcgcctc ccaacacgga tgtcatgggg atacgattcc cagaggtatc 480
gaatacatcc agcataatgg cgtcgtgcag gaaagctatt accgatacgt agctagggag 540
cagtcctgcc gccgtcctaa cgcacagcgc ttcggcattt ccaattattg ccagatctac 600
cccctaatg ccaacaagat cagggaggcc ctggcgcaga cgcacagcgc catcgctgtc 660
atcatcggaa tcaaggatct ggacgcattc cggcactatg acgggcgcac aatcatccag 720
cgcgacaacg gatatcagcc aaactaccac gcggtcaaca tcgtgggtta ctcgaacgcc 780
caggggtgg actactggat cgtgagaaac agttgggaca ctaactgggg cgacaacggc 840
tacggctact tcgccgccaa catcgacctg atgatgatcg aggagtaccc gtacgtggtg 900
atcctgtaa   909

<210> 2
<211> 302
<212> PRT
<213> Dermatophagoides pteronyssinus

<400> 2
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
 1   5   10   15
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

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            20                    25                    30
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
        35                    40                    45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
    50                    55                    60
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65                    70                    75                    80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
                85                    90                    95
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
            100                   105                   110
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
        115                   120                   125
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
    130                   135                   140
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile
145                   150                   155                   160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
                165                   170                   175
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
            180                   185                   190
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg
        195                   200                   205
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile
    210                   215                   220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
225                   230                   235                   240
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
                245                   250                   255
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
            260                   265                   270
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
        275                   280                   285
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
    290                   295                   300


<210> 3
<211> 302
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutant of ProDer P1 C4R  (Der P1 numbering)

<400> 3
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
 1               5                    10                   15
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
            20                    25                    30
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
        35                    40                    45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
    50                    55                    60
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65                    70                    75                    80
Thr Asn Ala Arg Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
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Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
            100   105   110
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
        115   120   125
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
    130   135   140
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile
145   150   155   160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
                165   170   175
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
            180   185   190
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg
        195   200   205
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile
    210   215   220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
225   230   235   240
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
                245   250   255
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
            260   265   270
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
        275   280   285
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
    290   295   300

<210> 4
<211> 909
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutant of ProDer P1 C4R (Der P1 numbering)

<400> 4
cggccgagct ccattaagac cttcgaggaa tacaagaaag ccttcaacaa gagctatgcc 60
accttcgagg acgaggaggc cgcgcgcaag aacttcctgg aaagcgtgaa atacgtgcag 120
agcaacggcg gggctataaa tcacctgtcc gacctgtctt tagacgagtt caagaaccgg 180
ttcctgatga gcgccgaggc tttcgaacac cttaagaccc agtttgatct caacgcggag 240
accaacgccc gtagtatcaa cggcaatgcc cccgctgaga ttgatctgcg ccagatgagg 300
accgtgactc ccatccgcat gcaaggcggc tgcgggtctt gttgggcctt ttcaggcgtg 360
gccgcgacag agtcggcata cctcgcgtat cggaatcaga gcctggacct cgctgagcag 420
gagctcgttg actgcgcctc ccaacacgga tgtcatgggg atacgattcc cagaggtatc 480
gaatacatcc agcataatgg cgtcgtgcag gaaagctatt accgatacgt agctagggag 540
cagtcctgcc gccgtcctaa cgcacagcgc ttcggcattt ccaattattg ccagatctac 600
cccccctaatg ccaacaagat cagggaggcc ctggcgcaga cgcacagcgc catcgctgtc 660
atcatcggaa tcaaggatct ggacgcattc cggcactatg acgggcgcac aatcatccag 720
cgcgacaacg gatatcagcc aaactaccac gcggtcaaca tcgtgggtta ctcgaacgcc 780
cagggggtgg actactggat cgtgagaaac agttgggaca ctaactgggg cgacaacggc 840
tacggctact cgccgccaa catcgacctg atgatgatcg aggagtaccc gtacgtggtg 900
atcctgtaa   909

<210> 5
<211> 302

<212> PRT
<213> Artificial Sequence

<220>
<223> Mutant of ProDer P1 C31R

<400> 5
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
 1   5   10   15
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
            20   25   30
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
        35   40   45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
    50   55   60
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65   70   75   80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
                85   90   95
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Arg Gly
            100   105   110
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
        115   120   125
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
    130   135   140
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile
145   150   155   160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
                165   170   175
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
            180   185   190
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg
        195   200   205
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile
    210   215   220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
225   230   235   240
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
                245   250   255
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
            260   265   270
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
        275   280   285
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
    290   295   300

<210> 6
<211> 909
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutant of ProDer P1 C31R

<400> 6
cggccgagct ccattaagac cttcgaggaa tacaagaaag ccttcaacaa gagctatgcc 60

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accttcgagg acgaggaggc cgcgcgcaag aacttcctgg aaagcgtgaa atacgtgcag  120
agcaacggcg gggctataaa tcacctgtcc gacctgtctt tagacgagtt caagaaccgg  180
ttcctgatga gcgccgaggc tttcgaacac cttaagaccc agtttgatct caacgcggag  240
accaacgcct gcagtatcaa cggcaatgcc cccgctgaga ttgatctgcg ccagatgagg  300
accgtgactc ccatccgcat gcaaggcggc cgtgggtctt gttgggcctt ttcaggcgtg  360
gccgcgacag agtcggcata cctcgcgtat cggaatcaga gcctggacct cgctgagcag  420
gagctcgttg actgcgcctc ccaacacgga tgtcatgggg atacgattcc cagaggtatc  480
gaatacatcc agcataatgg cgtcgtgcag gaaagctatt accgatacgt agctagggag  540
cagtcctgcc gccgtcctaa cgcacagcgc ttcggcattt ccaattattg ccagatctac  600
cccctaatg ccaacaagat cagggaggcc ctggcgcaga cgcacagcgc catcgctgtc  660
atcatcggaa tcaaggatct ggacgcattc cggcactatg acgggcgcac aatcatccag  720
cgcgacaacg gatatcagcc aaactaccac gcggtcaaca tcgtgggtta ctcgaacgcc  780
cagggggtgg actactggat cgtgagaaac agttgggaca ctaactgggg cgacaacggc  840
tacggctact cgccgccaa catcgacctg atgatgatcg aggagtaccc gtacgtggtg  900
atcctgtaa                                                          909
```

<210> 7
<211> 302
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutant of ProDer P1 C65R

<400> 7

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Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
  1               5                  10                  15
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
             20                  25                  30
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
         35                  40                  45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
     50                  55                  60
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
 65                  70                  75                  80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
                 85                  90                  95
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
             100                 105                 110
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
         115                 120                 125
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
     130                 135                 140
Arg Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile
145                 150                 155                 160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
                 165                 170                 175
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
             180                 185                 190
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg
         195                 200                 205
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile
     210                 215                 220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
225                 230                 235                 240
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
                 245                 250                 255
```

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Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
            260                 265                 270
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
        275                 280                 285
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
    290                 295                 300


<210> 8
<211> 909
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutant of ProDer P1 C65R

<400> 8
cggccgagct ccattaagac cttcgaggaa tacaagaaag ccttcaacaa gagctatgcc 60
accttcgagg acgaggaggc cgcgcgcaag aacttcctgg aaagcgtgaa atacgtgcag 120
agcaacggcg gggctataaa tcacctgtcc gacctgtctt tagacgagtt caagaaccgg 180
ttcctgatga cgcgccgagg ctttcgaaca cttaagaccc agtttgatct caacgcggag 240
accaacgcct gcagtatcaa cggcaatgcc cccgctgaga ttgatctgcg ccagatgagg 300
accgtgactc ccatccgcat gcaaggcggc tgcgggtctt gttgggcctt ttcaggcgtg 360
gccgcgacag agtcggcata cctcgcgtat cggaatcaga gcctggacct cgctgagcag 420
gagctcgttg accgtgcctc ccaacacgga tgtcatgggg atacgattcc cagaggtatc 480
gaatacatcc agcataatgg cgtcgtgcag gaaagctatt accgatacgt agctagggag 540
cagtcctgcc gccgtcctaa cgcacagcgc ttcggcattt ccaattattg ccagatctac 600
cccccctaatg ccaacaagat cagggaggcc ctggcgcaga cgcacagcgc catcgctgtc 660
atcatcggaa tcaaggatct ggacgcattc cggcactatg acgggcgcac aatcatccag 720
cgcgacaacg gatatcagcc aaactaccac gcggtcaaca tcgtgggtta ctcgaacgcc 780
cagggggtgg actactggat cgtgagaaac agttggggaca ctaactgggg cgacaacggc 840
tacggctact tcgccgccaa catcgacctg atgatgatcg aggagtaccc gtacgtggtg 900
atcctgtaa                                                     909


<210> 9
<211> 302
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutant of ProDer P1 C71R

<400> 9
Arg Pro Ser Ser Ile Lys Thr Phe Glu Glu Tyr Lys Lys Ala Phe Asn
 1                5                  10                  15
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
            20                  25                  30
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
        35                  40                  45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
    50                  55                  60
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
65                  70                  75                  80
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
                85                  90                  95
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
            100                 105                 110
```

Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
         115   120   125
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
         130   135   140
Cys Ala Ser Gln His Gly Arg His Gly Asp Thr Ile Pro Arg Gly Ile
145   150   155   160
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
                 165   170   175
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
                 180   185   190
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg
         195   200   205
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile
         210   215   220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
225   230   235   240
Arg Asp Asn